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OM protein - protein search, using sw model
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Perfect score:
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
pir1:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT S67482

Db 241 IGAGSCILGNITIGEGAKIGSGSVVVALVFA Qy 301 DQTSXLTEWSDYVI 314	QY 181 VDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVFLGGTGKQSGDRHPKIGDGVL	QY 61 KQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNT_FELFISVLEESPEIIEST	Query Match 100.0%; Score 1641; DB 2; Length 314; Best Local Similarity 100.0%; Pred. No. 8.8e-129; Best Local Similarity 100.0%; Pred. No. 8.8e-129; Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Indels 0; G: Matches 314; Conservative 0; Mismatches 0; Mismatches 0; G: Matches 314; Conservative 0; Mismatches 0; Mismatches 0; G: Matches 314; Conservative 0; Mismatches 0; Mismatc	A; Accession: 507702 A; Mclecule type: DNA A; Residues: 1-314 <rue> A; Residues: 1-314 <rue> A; Residues: 1-314 <rue> A; Cross-references: EMBL: 234888; NID: 9608676; PIDN: CAA84371.1; PID: 9608677 A; Cross-references: EMBL: 234888; NID: 9608676; PIDN: CAA84371.1; PID: 9608677 A; Note: the authors translated the codon ACC for residue 158 as Ile and ACA A; Note: the authors translated the codon ACC for residue 158 as Ile and ACA A; Note: the authors explicated the codon ACC for residue 158 as Ile and ACA C; Superfamily: serine acetyltransferase; serine acetyltransferase homology <sat> F; 123-283/Domain: serine acetyltransferase homology <sat></sat></sat></rue></rue></rue>	c; Species: Arabidopsis charten (Nouse Cr. Species) Arabidopsis charten (Nouse Cr. Spe	S67482 serine O-acetyltransferase (EC 2.3.1.30), cytosolic - Arabidopsis thaliana N;Alternate names: serine acetyltransferase
NT TO A GREEN STREET	NVSILHGV7LGGTGKQSGDRHPKIGDGVL 240	LSNINLPSNT_FELFISVLEESPEIIEST 120		8676; PIDN:CAA84371.1; PID:g608677 ACC for residue 158 as Ile and ACA for resid serine acc:yltransferase homology cysteine biosynthesis se homology <sat></sat>	Apr.1997 #text_change 05-May-2000 ce, R. e acety tiansferase from Pisum sativum and	cytosolic - Arabidopsis thaliana e cress)

C;Superfamily: serine acetyltransferase; serine acetyltransferase homology (;Keywords: acyltransferase; chloroplast; coenzyme A; cysteine biosynthesis F;1-60/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;61-391/Product: serine O-acetyltransferase SAT-la, chloroplast #status predicted <M

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A;Cross-references:
C;Genetics:
                                        A; Molecule type: mRNA
A; Residues: 80-391 <HEL>
                                                                                        A; Reference number: S71906
A; Accession: S71906
                                                                                                                             submitted to the EMBL Data Library, July 1995
                                                                                                                                                                 A;Cross-references: EMBL:U22964; NID:g1184047; PIDN:AAB07778.1; PID:g1184048
                                                                                                                                                                                                                                                           R;Roberts, M.A.; Wray, J.L.
Plant Mol. Biol. 30, 1041-1049, 1996
A;Title: Cloning and characterisation of an Arabidopsis thaliana cDNA clone encoding an A;Reference number: $69192; MUID:96270381
                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-391 < ROB>
                                                                                                                                                                                                                                                                                                                                                        serine O-acetyltransferase (EC 2.3.1.30) SAT-la precursor, chloroplast - Arabidopsis that C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Dec-1996 #sequence_revision 27-Feb-1997 #text_change 05-May-2000
C;Accession: S69192; S71906
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A; Accession: S71181
A; Accelle type: mRNA
A; Modelle type: mRNA
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:L42212; NID:g926938; PIDN:AAC37474.1; PID:g926939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-314 <MUR>
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A;Description: Analysis of a cDNA encoding serine acetyltransferase from Arabidopsis tha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KQEPILSNYYYASITSHRSLESALGHILSVKLSNLNLPSNTLFELFISVLEESPEIIEST
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EMBL: x82888; NID: g897677; PIDN: CAA58061.1; PID: g897678
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c;Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
F;113-272/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Title: Cysteine biosynthesis in plants: isolatic and functional identification of A;Reference number: S68469; MUID:95121457
A;Accession: S68469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-303 < BOG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            c:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 15-Feb-197 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
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                                                                                                                                                                                                                                                                               Matches 222;
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122 PACISYVHCFLHFKGFLACQAHRIAHELWTQDRKILALLIQNRVSEAFAVDFHPGAKIGT 181
                       132 PACISYVHCFLGFKGFLACQAHRIAHTLMKQNRKIVALLIQNRVSESFAVDIHPGAKIGK 191
                                                                                     62 ASIVSQRSYEAALANTLSVKLSNLNLPSNTLFDLFSGVLQGNPDIVESVKLDLLAVKERD
                                                                                                                             72 ASITSHRSLESALAHILSVKLSNLNLPSNTLFELFISVLEESPEIIESTKQDLIAVKERD 131
                                                                                                                                                                                                                 25 NFFR-PGFS----VNRKIHHTQ--IED-----DDDVWIKMLEEAKSDVKQEPILSNYYY 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 LWTQDRKILALLIQNRVSEAFAVDFHPGAKIGTGILLDH?, `AIVIGETAVVGNNVSILHN
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                                                                                                                                                                       NYFRYPDRSSFNGTQTKTLHTRPLLEDLDRDAEVDDVWAKIKEEAKSDIAKEPIVSAYYH 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTLGGTGKQCGDRHPKIGDGVLIGAGTCILGNITIGEGAE GAGSVVLKDVPPRTTAVGN 355
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                                                                                                                                                                                                                                                                                      67.3%; Score 1105; DB 2; Length 303; 73.0%; Pred. No. 2.8e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.0%; Score 1215; DB 2; Length 391; 72.0%; Pred. No. 2.9e-93;
                                                                                                                                                                                                                                                                 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Mismatches
                                                                                                                                                                                                                                                                    36; Indels
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                                                                                                                                                                                                                                                               16;
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                                                                                                                                                                                                                                                             Gaps
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C;Species: Spinacia oleracea (spinach)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δõ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:D88529
A;Experimental source: leaf
C;Function:
A;Description: catalyzes conversion of L-serine to O-acetyl serine (by acetyl CoA)
A;Pathway: cysteine biosynthesis
A;Pathway: cysteine biosynthesis
C;Superfamily: serine acetyltransferase; serine acetyltransferase; cysteine biosynthesis
C;Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
F;156-316/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serine O-acetyltransferase (EC 2.3.1.30) - spinach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: 216582
A; Accession: T09140
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serine O-acetyltransferase (EC 2.3.1.30) - watermelon C;Species: Citrullus lanatus (watermelon)  
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 20-Jun-2000 C;Caccession: A57478  
R;Saito, K.; Yokoyama, H.; Noji, M.; Murakoshi, I.
J. Biol. Chem. 270, 16321-16326, 1995
A;Title: Molecular cloning and characterization of a plant serine acetyltransferase play A;Reference number: A57478; MUID:95332343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 ITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKENPRKHDKIPCLTMDQTSYLTEWS 310
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                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                  267 KDVPARTTAVGNPARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 ILSVKLSNINLPSNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 PG--FSVNRKIHHTQIEDDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAH 86
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                                                                                                                                                                                                                                                                                                                                                                                                                        AIIGDNCSILHHVTLGGTGKAGGDRHPKVGDGVLIGAGATILGNVRIGDGAKIGAGSVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGGDLSVAPSVGHLTANNEAWLWDQIKGEARRDADSEPALASYLYSTILSHSSLERSLSF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLACQSHRVAHKLWNQDRRPLALALHSRISDVFAVDIHPAARIGKGILFDHATGVVIGET 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLACQAHRIAHTLWKONRKIVALLIONRVSESFAVDIHPGAKIGKGILLDHATGVVIGET 206
                                                                                                                                                                                                                                                                                                                       IDVPPRTTAVGNPARLIGGKEKPSQNSDVPGESMDHTSFISEWSDYII 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takagi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.4%; Score 877; DB 2; 56.6%; Pred. No. 2.9e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
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C;Superfamily: serine acetyltransferase; serine acetyltransferase C;Keywords: acyltransferase; coenzyme A F;103-263/Domain: serine acetyltransferase homolo- <SAT>
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A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-294 <SAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serine O-acetyltransferase (EC 2.3.1.30) Sat-52 - A-abidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress); C;Date: 19 Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000 C;Accession: $71207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: serine acetyltransferase; serine ac:tyltransferase homology C;Keywords: acyltransferase; coenzyme A; cysteine liosynthesis F;120-280/Domain: serine acetyltransferase homology <SAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-312 <HOW>
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A; Accession: S71207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 GNPARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 3+1
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                                                                                                                                                                                         105 NTESSDPSLRNATVADLRAARVRDPACISESHCLLNYKGF ATQAHRVSHKLWTQSRKPL 164
225 CGDRHPKIGDGCLIGAGATILGNVKIGAGAKVGAGSVVLTIVPCRGTAVGNPARLVGGKE 284
                                         228 SGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKE
                                                                                                                                                                                                                                                                                           45 LWTQIKAEARRDAEAEPALASYLYSTILSHSSLERSISFH GNKLCSSTLLSTLLYDLFL 104
                                                                                                                                                                                                                                                                                                                                          48 WIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHIUSVKLSNLNLPSNTLFELFI 107
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                           ALLIQURVSESFAVDIHPGAKIGKGILLDHATGVVIGETA VSDNVSILHGVTLGGTGKO 227
                                                                                                                                                                                                                                          SVLEESPEIIESTKODLIAVKERDPACISYVHCFLGFKGF "ACQAHRIAHTLWKONRKIV 167
                                                                                               ALALHSRISDVFAVDIHPAAKIGKGILLDHATGVVVGET; · ¡GNNVSILHHVTLGGTGKA 224
                                                                                                                                                                                                                                                                                                                                                                                                160;
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58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                          51.8%; Score 849.5; DB 2
59.7%; Pred. No. 4.9e-63;
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Pred. No. 1.
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A;Cross-references: GB:AE002412; GB:AE002098; NID:g7225783; PIDN:AAF40988.1; PID:g722578
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
                                                                                                                                                                                                                                                                                                        R.Tettelin, H.; Saunders, N.J.; Heldelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-272 <TET>
                                                                                                                                                                                                                                                                             A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58
                                                                                                                                                                                                            A:Status: preliminary
                                                                                                                                                                                                                                                 A; Reference number: A81000; MUID: 20175755
A; Accession: C81184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable serine O-acetyltransferase (EC 2.3.1.30) NMA0742 [imported] - Neisseria meningi C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001 C;Accession: C81184; H81917
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A; Residues: 1-315 <STO>
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N;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable serine acetyltransferase [imported] - Arabidopsis thaliana (¿Species: Arabidopsis thaliana (mouse-ear cress) (¿Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: F84554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 GSGSVVVKDVPARTTAVGNPARLIGGKENPRKHDKIPCLTM 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 GVVIGETAVIGNGVSILHGVTLGGTGKETGDRHPKIGEGALLGACVTILGNISIGAGAMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 GVVIGETAVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 AILHLKGYHALQAYRVAHKLWNEGRKLLALALQSRISEVFGIDIHPAARIGEGILLDHGT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 CFLGFKGFLACQAHRIAHTLWKQNRKIVALLIQNRVSESFAVDIHPCAKIGKGILLDHAT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 LEQALGEVLANRLQNPTLLATQLLDIFYGVMMHDKGIQSSIRHDLQAFKDRDPACLSYSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 LESALAHILSVKLSNLNLPSNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVH 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 42.6%;
Local Similarity 50.2%;
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Pred. No. 1.6e-50;
50; Mismatches 76; Indels
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A;Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18584.1; PID:g466745 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Peria, N.T.; Burland, V.; .A.; Rose, D.J.; Mau, B.; Shao, Y.
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A;Cross-references: GB:M15745; NID:9145675; PIDN:AAA23648.1; PID:9145676
R;Tei, H.; Murata, K.; Kinura, A.
Biochem. Blophys. Res. Commun. 167, 948-955, 1990
A;Title: Structure and expression of CYSX, the second gene in the Escherichia coli K-A;Reference number: A34563; MUID:90211342
A; Molecule type: DNA
A; Residues: 1-273 < PLU>
                                                    A;Reference number: A;Accession: S47828
                                                                                          submitted to the EMBL Data Library, March 1994
                                                                                                                                    R;Plunkett,
                                                                                                                                         A;Cross-references: GB:M34333; NID:gl45693; PIDN:AAA23659.1; PID:gl45694
                                                                                                                                                                                                                                                                                                                                                                                                                         R;Denk, D.; Bock, A.
J. Gen. Microbiol. 133, 515-525, 1987
A;Title: L-Cysteine biosynthesis in Escherichia coll: nucleotide sequence and express A;Reference number: A27896; MUID:88009872
A;Accession: A27896
                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-273 <TEI>
                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-273 <DEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serine O-acetyltransferase (EC 2.3.1.30) - Escherichia coli
C;Species: Escherichia coli
C;Date: 30-Jun-1988 #sequence_revision_30-Jun-1988 #text_change 05-May-2000
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A;Reference number: A81775; MUID:20222556
A;Accession: H81917
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Nature 404, 502-506, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 QSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGK 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 ISVLEESPEIIESTKODLIAVKERDPACISYVHCFLGFKSFLACQAHRIAHTLWKQNRKI 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 DLWHTIREETAAAVSAEPMLASFLHQTVLRHESLGSVLAYHLSSKLGSPIMDVRALFEIY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 DVWIKMLEEAKSDVKQEPILSNYYYASTTSHRSLESALAHILSVKLSNLNLPSNTLFELF 106
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Local Similarity 50.7%; Pred. No. 1.7
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                                                                                                                                    G.
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Riley, M.;

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A; Molecule type: DNA
A; Residues: 1-273 <SIV>
A; Residues: 1-273 <SIV>
A; Cross references: EMBL:X59594; NID:g47659; PIDN:CAA42163.1; PID:g47660
C; Superfamily: serine acetyltransferase; serine acetyltransferase homology
C; Keywords: acyltransferase; coenzyme A
C; Keywords: acyltransferase; coenzyme A
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A;Description: A novel biosynthetic pathway for mammalian cells by stable integration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000 C:Accession: S29568 R:Sivaprasad, A.V.; Kuczek, E.S.; Bawden, C.S.; Rogers, G.E.
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A; Accession: S29568
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A;Reference number: A64720; MUID:97426617
A;Accession: A65161
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-273 <BLAT>
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A; Title: The complete genome
                                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                     Query Match
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                                               103 FELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQ 162
64 REVVEEAYAADPEMIASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWNK 123
                                                                                                                                            43 EDDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 VGKPDS----DK-PSMDMDQ 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 NRKIVALLIONRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSTLHGVTLG 222
                                                                                               4 EELEIVWKNIKAEARALADCEPMLASFYHATLLKHENLGSALSYMLANKLASPIMPAIAI 63
                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 REVVEEAYAADPEMIASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 EELEIVWNNIKAEARTLADCEPMLASFYHATLLKHENLGSALSYMLANKLSSPIMPAIAI 63
                                                                                                                                                                                                          133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGKSGGDRHPKIREGVMIGAGAKILGNIEVGRGAKIGAGSVVLQPVPPHTTAAGVPARI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGKQSGDRHPKIGDGYLIGAGSCILGNITIGEGAKIGSGSVYVKDVPARTTAVGNPARL
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                                                                                                                                                                                                   50; Mismatches
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                                                                                                                                                                                                                       Score 648.5; DB Pred. No. 2e-46;
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                           A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae
A; Reference
                                                                                                                                                                                      C; Species: Vibrio cholerae
                                                                                                                                                                                           serine acetyltransferase VC2649 [imported] - Vibri cholerae (strain N16961 serogroup
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A; Molecule type: DNA
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F86036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene:
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                             283 IGGKENPRKHDKIPCLTMDQ 302
                                                                                184 GTGKSGGDRHPKIREGVMIGAGAKILGNIEVGRGAKIGAGSVVLQPVPPHTTAAGVPARI 243
244 VGKPDS----DK-PSMDMDQ 258
                                                                                                                                                                                                       163 NRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLG
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                                                                                                                                                                            GRRALAIFLQNQVSVTFQVDIHPAAKIGRGIMLDHATGIVVGETAVIENDVSILQSVTLG 183
                                                                                                                                                                                                                                                                        REVVEEAYAADPEMIASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWNQ 123
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Pred. No. 2e-46;
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number: A82035; MUID:20406833

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A;Gene: VC2649
A;Map position: 1
C;Superfamily: serine acetyltransferase; serine acetyltransferase homology
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-273 <HEI>
A;Cross-references: GB:AE004331; GB:AE003852; NID:g9657236; PIDN:AAF95790.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AF024504; NID:g2435510; PID:g2435513; GSPDB:GN00062; ATSP:A_TMCA;Experimental source: cultivar Columbia; BAC clone TM017A05
C;Genetics:
A;Gene: ATSP:A_TM017A05.1
A;Map position: 4
A;Introns: 47/3; 113/3; 139/2; 181/1; 212/3; 273/2; 298/1
C;Superfamily: serine acetyltransferase; serine acetyltransferase homology
C;Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
F;111-283/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serine O-acetyltransferase (EC 2.3.1.30) A_TM017A05.1 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-May-2000 C;Accession: T08867
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A;Molecule type: DNA
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A; Accession: T08867
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 AMAVREVIEEAFAADPSISEAAACDICATVNRDPAVSMYSMPLLYLKGYHALQGYRVANW 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTK-----VWQTIVAEAREQAEQEPMLASFYHATIIKHDSLKAALSYILANRLNTASMP 59
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                                         LESALAHILSVKLSNLNLPSNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVH 139
                                                                                                                               FRPGFSVNRK-IHHTQIEDD------DDVWIKMLEEAKSDVKQEPILSNYYYASITSHRS 79
                                                                                      FESGFEVYAKGTHKSEFDSNLLDPRSDPIWDAIREEAKLEAEKEPILSSFLYAGILAHDC 67
LEQALGFYLANRLQNPTLLATQLLDIFYGYMMHDKGIQSSIRHDLQAFKDRDPACLSYSS 127
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45.2%;
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                                                                                                                                                                                                 Score 643; DB 2;
Pred. No. 6.8e-46;
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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayto, R.A.; Kirkness, E.F.; Kerlavage; Godayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I. Glodek, A.; Kelley, J.M.; Weldman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serine O-acetyltransferase (EC 2.3.1.30) - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: serine acetyltransferase; serine acetyltransferase homology C;Keywords: acyltransferase; coenzyme A; cysteine biosynthesis F;80-240/Domain: serine acetyltransferase homology <SAT>
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A; Residues: 1-267 <TIGR>
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Best Local Similarity
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                                                                                                                                     OSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGK 286
----SQDKAAKPAFDMNQ
                                          ENPRKHDKI -- PCLTMDQ 302
                                                                                             ESGDRHPKVREGVMIGAGAKILGNIEVGKYAKIGANSVVL!! VPEYATAAGVPARIV---
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